

## SEQUENCE LISTING

<110> Hudson et al.  
 <120> Human Choline Acetyltransferase  
 <130> PF146P1D3  
 <150> US 09/939,573  
 <151> 2001-08-28  
 <150> US 09/210,993  
 <151> 1998-12-15  
 <150> US 08/464,601  
 <151> 1995-06-05  
 <150> PCT/US94/13570  
 <151> 1994-11-23  
 <160> 8  
 <170> PatentIn version 3.1  
 <210> 1  
 <211> 2034  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> (1)..(2034)  
 <223>  
 <400> 1

atg aag gct tcc agc cgc ttc aag gca cac cag gat gca ctg cca cgg	48		
Met Lys Ala Ser Ser Arg Phe Lys Ala His Gln Asp Ala Leu Pro Arg			
1	5	10	15
ttg ccc gtg ccc cct ctc cag cag tcc ctg gac cac tac ctg aag gcg	96		
Leu Pro Val Pro Pro Leu Gln Gln Ser Leu Asp His Tyr Leu Lys Ala			
20	25	30	
ctg cag ccc atc gtg agt gag gag tgg gcc cac acc aag cag ctg	144		
Leu Gln Pro Ile Val Ser Glu Glu Trp Ala His Thr Lys Gln Leu			
35	40	45	
gtg gat gag ttt cag gcc tca gga ggt gta ggg gag cgc ctg cag aag	192		
Val Asp Glu Phe Gln Ala Ser Gly Gly Val Gly Glu Arg Leu Gln Lys			
50	55	60	
ggg ctg gag cgt cgg gcc agg aag acg gag aac tgg ctg tct gag tgg	240		
Gly Leu Glu Arg Arg Ala Arg Lys Thr Glu Asn Trp Leu Ser Glu Trp			
65	70	75	80
tgg ctc aag acc gcc tac ctc cag tac cgc cag cct gtg gtc atc tac	288		
Trp Leu Lys Thr Ala Tyr Leu Gln Tyr Arg Gln Pro Val Val Ile Tyr			
85	90	95	

tcg agc cca ggc gtg atg cta ccc aag cag gac ttc gtg gac ctg cag Ser Ser Pro Gly Val Met Leu Pro Lys Gln Asp Phe Val Asp Leu Gln 100 105 110	336
ggt cag ctc cga ttt gct gcc aaa ctc att gag ggt gtg ttg gtt ttc Gly Gln Leu Arg Phe Ala Ala Lys Leu Ile Glu Gly Val Leu Val Phe 115 120 125	384
aag gtc atg att gac aac gag acc ctg ccc gtg gag tac ctg ggg ggg Lys Val Met Ile Asp Asn Glu Thr Leu Pro Val Glu Tyr Leu Gly Gly 130 135 140	432
aag cca ctg tgc atg aac cag ttc tat cag atc ttg tcc tcc tgc cga Lys Pro Leu Cys Met Asn Gln Phe Tyr Gln Ile Leu Ser Ser Cys Arg 145 150 155 160	480
gtg ccg ggc ccc aag cag gac aca gtc agc aac ttc agc aag acc aag Val Pro Gly Pro Lys Gln Asp Thr Val Ser Asn Phe Ser Lys Thr Lys 165 170 175	528
aag cct ccc acg cac atc acc gtg gta cac aac tac cag ttt ttt gag Lys Pro Pro Thr His Ile Thr Val Val His Asn Tyr Gln Phe Phe Glu 180 185 190	576
ctg gat gtg tac cac agt gac ggg aca ccc ctc act gcg gat cag atc Leu Asp Val Tyr His Ser Asp Gly Thr Pro Leu Thr Ala Asp Gln Ile 195 200 205	624
ttt gtg cag ctg gag aag atc tgg aac tca tcc cta cag acc aac aag Phe Val Gln Leu Glu Lys Ile Trp Asn Ser Ser Leu Gln Thr Asn Lys 210 215 220	672
gag cct gtg ggc atc ctc acc tcc aac cac cgc aac tcc tgg gcc aag Glu Pro Val Gly Ile Leu Thr Ser Asn His Arg Asn Ser Trp Ala Lys 225 230 235 240	720
gca tac aac acc ctc atc aaa gac aag gtg aac cgg gat tcc gtg cgc Ala Tyr Asn Thr Leu Ile Lys Asp Lys Val Asn Arg Asp Ser Val Arg 245 250 255	768
tcc atc cag aag agc atc ttc acc gtg tgc cta gat gca acc atg ccc Ser Ile Gln Lys Ser Ile Phe Thr Val Cys Leu Asp Ala Thr Met Pro 260 265 270	816
agg gtc tca gaa gac gtg tac cgc agc cac gtg gca ggc cag atg ctg Arg Val Ser Glu Asp Val Tyr Arg Ser His Val Ala Gly Gln Met Leu 275 280 285	864
cat ggg ggc ggc agc agg ctc aac agc ggc aac cgc tgg ttc gac aag His Gly Gly Ser Arg Leu Asn Ser Gly Asn Arg Trp Phe Asp Lys 290 295 300	912
acg ctg cag ttc atc gtg gca gaa gat ggc tcc tgt ggg ctt gtg tac Thr Leu Gln Phe Ile Val Ala Glu Asp Gly Ser Cys Gly Leu Val Tyr 305 310 315 320	960
gag cat gct gca gcg gag ggg ccc cct att gtc acc ctt ctg gac tat Glu His Ala Ala Ala Glu Gly Pro Pro Ile Val Thr Leu Leu Asp Tyr 325 330 335	1008

gtc atc gag tac acg aag aaa ccc gag ctt gtg cggtatccatggtg Val Ile Glu Tyr Thr Lys Lys Pro Glu Leu Val Arg Ser Pro Met Val 340 345 350	1056
ccc ctg ccc atg ccc aag aag ctg cggttccaaatccccc gag atc Pro Leu Pro Met Pro Lys Lys Leu Arg Phe Asn Ile Thr Pro Glu Ile 355 360 365	1104
aag agc gac atc gag aag gcc aag cag aac ctc agc atc atg atc cag Lys Ser Asp Ile Glu Lys Ala Lys Gln Asn Leu Ser Ile Met Ile Gln 370 375 380	1152
gac ctg gat atc acc gtg atg gtg ttc cac cat ttt gga aaa gac ttc Asp Leu Asp Ile Thr Val Met Val Phe His His Phe Gly Lys Asp Phe 385 390 395 400	1200
ccc aag tcg gag aag cta agc cca gat gcc ttc atc cag atg gct ttg Pro Lys Ser Glu Lys Leu Ser Pro Asp Ala Phe Ile Gln Met Ala Leu 405 410 415	1248
cag ctg gcc tac tac agg ttc tac gga aag gaa tgt gcc acc tat gaa Gln Leu Ala Tyr Tyr Arg Phe Tyr Gly Lys Glu Cys Ala Thr Tyr Glu 420 425 430	1296
agt gcc tcc ctg cgc atg ttt cac ctg ggg cgc acc gac acc atc cgc Ser Ala Ser Leu Arg Met Phe His Leu Gly Arg Thr Asp Thr Ile Arg 435 440 445	1344
tcg ggt tcc atg gac tca ctc acc ttt gtc aag gcc atg gat gac tcc Ser Gly Ser Met Asp Ser Leu Thr Phe Val Lys Ala Met Asp Asp Ser 450 455 460	1392
agc gtc acg gag cac cag aag gtg gag ctg ctg cgg aag gcc gtg cag Ser Val Thr Glu His Gln Lys Val Glu Leu Leu Arg Lys Ala Val Gln 465 470 475 480	1440
gcc cac cga ggt tac acc gac cgg gcc atc cgg ggg gag ggc ttt gat Ala His Arg Gly Tyr Thr Asp Arg Ala Ile Arg Gly Glu Gly Phe Asp 485 490 495	1488
cga cac ctg ctg ggc ctg aag ctg cag gcc atc gag gac ctg gtg agc Arg His Leu Leu Gly Leu Lys Leu Gln Ala Ile Glu Asp Leu Val Ser 500 505 510	1536
atg ccc gac atc ttc atg gac acc tcc tac gcc atc ggc atg tac ttc Met Pro Asp Ile Phe Met Asp Thr Ser Tyr Ala Ile Gly Met Tyr Phe 515 520 525	1584
cac ctc tcc acc agg cag gtc cct gcc aag aag atg tgt cat gtt ctt His Leu Ser Thr Arg Gln Val Pro Ala Lys Lys Met Cys His Val Leu 530 535 540	1632
cgg gcc cgt ggt ccc cga cgg gta cgg tgt ctt tat aac ccc atg gag Arg Ala Arg Gly Pro Arg Arg Val Arg Cys Leu Tyr Asn Pro Met Glu 545 550 555 560	1680
ggc cac atc aac ttc tcc ctg tcg gac tac aaa agg tgg ggg gag acc Gly His Ile Asn Phe Ser Leu Ser Asp Tyr Lys Arg Trp Gly Glu Thr 565 570 575	1728

aac gcc gcc cgc ctg gtg tat tac ctg gag aag gcg ctc ctg gac atg Asn Ala Ala Arg Leu Val Tyr Tyr Leu Glu Lys Ala Leu Leu Asp Met 580	585	590	1776
cgt gcc ctg gtg aag agc cac ccc cg <sup>g</sup> gcc aag ttc tta gcc cct agg Arg Ala Leu Val Lys Ser His Pro Arg Ala Lys Phe Leu Ala Pro Arg 595	600	605	1824
act cag gcc tgc caa tgc cac agg caa gcc cac cct agg atg ggc cac Thr Gln Ala Cys Gln Cys His Arg Gln Ala His Pro Arg Met Gly His 610	615	620	1872
cca cca ggg atc agc tcc ttg gtt ccc tct tcc ttg gtt ccc tct tcc Pro Pro Gly Ile Ser Ser Leu Val Pro Ser Ser Leu Val Pro Ser Ser 625	630	635	1920
ctg gtc ccc cca att cta ctg agc cac gga ccg cat cct cca ggg ggc Leu Val Pro Pro Ile Leu Leu Ser His Gly Pro His Pro Pro Gly Gly 645	650	655	1968
tgc agg ccc agc caa gtg cct tcc gtg ggt cat ccc agc acc tgc cag Cys Arg Pro Ser Gln Val Pro Ser Val Gly His Pro Ser Thr Cys Gln 660	665	670	2016
ggc ccg acc tgg ggc tga Gly Pro Thr Trp Gly 675			2034
<210> 2 <211> 677 <212> PRT <213> Homo sapiens			
<400> 2			
Met Lys Ala Ser Ser Arg Phe Lys Ala His Gln Asp Ala Leu Pro Arg 1 5 10 15			
Leu Pro Val Pro Pro Leu Gln Gln Ser Leu Asp His Tyr Leu Lys Ala 20 25 30			
Leu Gln Pro Ile Val Ser Glu Glu Glu Trp Ala His Thr Lys Gln Leu 35 40 45			
Val Asp Glu Phe Gln Ala Ser Gly Gly Val Gly Glu Arg Leu Gln Lys 50 55 60			
Gly Leu Glu Arg Arg Ala Arg Lys Thr Glu Asn Trp Leu Ser Glu Trp 65 70 75 80			
Trp Leu Lys Thr Ala Tyr Leu Gln Tyr Arg Gln Pro Val Val Ile Tyr 85 90 95			

Ser Ser Pro Gly Val Met Leu Pro Lys Gln Asp Phe Val Asp Leu Gln  
100 105 110

Gly Gln Leu Arg Phe Ala Ala Lys Leu Ile Glu Gly Val Leu Val Phe  
115 120 125

Lys Val Met Ile Asp Asn Glu Thr Leu Pro Val Glu Tyr Leu Gly Gly  
130 135 140

Lys Pro Leu Cys Met Asn Gln Phe Tyr Gln Ile Leu Ser Ser Cys Arg  
145 150 155 160

Val Pro Gly Pro Lys Gln Asp Thr Val Ser Asn Phe Ser Lys Thr Lys  
165 170 175

Lys Pro Pro Thr His Ile Thr Val Val His Asn Tyr Gln Phe Phe Glu  
180 185 190

Leu Asp Val Tyr His Ser Asp Gly Thr Pro Leu Thr Ala Asp Gln Ile  
195 200 205

Phe Val Gln Leu Glu Lys Ile Trp Asn Ser Ser Leu Gln Thr Asn Lys  
210 215 220

Glu Pro Val Gly Ile Leu Thr Ser Asn His Arg Asn Ser Trp Ala Lys  
225 230 235 240

Ala Tyr Asn Thr Leu Ile Lys Asp Lys Val Asn Arg Asp Ser Val Arg  
245 250 255

Ser Ile Gln Lys Ser Ile Phe Thr Val Cys Leu Asp Ala Thr Met Pro  
260 265 270

Arg Val Ser Glu Asp Val Tyr Arg Ser His Val Ala Gly Gln Met Leu  
275 280 285

His Gly Gly Ser Arg Leu Asn Ser Gly Asn Arg Trp Phe Asp Lys  
290 295 300

Thr Leu Gln Phe Ile Val Ala Glu Asp Gly Ser Cys Gly Leu Val Tyr  
305 310 315 320

Glu His Ala Ala Ala Glu Gly Pro Pro Ile Val Thr Leu Leu Asp Tyr  
325 330 335

Val Ile Glu Tyr Thr Lys Lys Pro Glu Leu Val Arg Ser Pro Met Val  
340 345 350

Pro Leu Pro Met Pro Lys Lys Leu Arg Phe Asn Ile Thr Pro Glu Ile  
355 360 365

Lys Ser Asp Ile Glu Lys Ala Lys Gln Asn Leu Ser Ile Met Ile Gln  
370 375 380

Asp Leu Asp Ile Thr Val Met Val Phe His His Phe Gly Lys Asp Phe  
385 390 395 400

Pro Lys Ser Glu Lys Leu Ser Pro Asp Ala Phe Ile Gln Met Ala Leu  
405 410 415

Gln Leu Ala Tyr Tyr Arg Phe Tyr Gly Lys Glu Cys Ala Thr Tyr Glu  
420 425 430

Ser Ala Ser Leu Arg Met Phe His Leu Gly Arg Thr Asp Thr Ile Arg  
435 440 445

Ser Gly Ser Met Asp Ser Leu Thr Phe Val Lys Ala Met Asp Asp Ser  
450 455 460

Ser Val Thr Glu His Gln Lys Val Glu Leu Leu Arg Lys Ala Val Gln  
465 470 475 480

Ala His Arg Gly Tyr Thr Asp Arg Ala Ile Arg Gly Glu Gly Phe Asp  
485 490 495

Arg His Leu Leu Gly Leu Lys Leu Gln Ala Ile Glu Asp Leu Val Ser  
500 505 510

Met Pro Asp Ile Phe Met Asp Thr Ser Tyr Ala Ile Gly Met Tyr Phe  
515 520 525

His Leu Ser Thr Arg Gln Val Pro Ala Lys Lys Met Cys His Val Leu  
530 535 540

Arg Ala Arg Gly Pro Arg Arg Val Arg Cys Leu Tyr Asn Pro Met Glu  
545 550 555 560

Gly His Ile Asn Phe Ser Leu Ser Asp Tyr Lys Arg Trp Gly Glu Thr  
565 570 575

Asn Ala Ala Arg Leu Val Tyr Tyr Leu Glu Lys Ala Leu Leu Asp Met  
580 585 590

Arg Ala Leu Val Lys Ser His Pro Arg Ala Lys Phe Leu Ala Pro Arg  
595 600 605

Thr Gln Ala Cys Gln Cys His Arg Gln Ala His Pro Arg Met Gly His  
610 615 620

Pro Pro Gly Ile Ser Ser Leu Val Pro Ser Ser Leu Val Pro Ser Ser  
625 630 635 640

Leu Val Pro Pro Ile Leu Leu Ser His Gly Pro His Pro Pro Gly Gly  
645 650 655

Cys Arg Pro Ser Gln Val Pro Ser Val Gly His Pro Ser Thr Cys Gln  
660 665 670

Gly Pro Thr Trp Gly  
675

<210> 3  
<211> 34  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains a BamHI restriction enzyme site

<400> 3  
cgcgagatcc accatgaagg cttccagccg cttc 34

<210> 4  
<211> 28  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains complementary sequences to an XbaI site

<400> 4  
cgcgtctaga agggtacaga tggtgcc 28

<210> 5  
<211> 34  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains a Bam H1 restriction enzyme site

<400> 5  
cgcgggatcc accatgaagg cttccagccg cttc

34

<210> 6  
<211> 27  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains the cleavage site for the restriction endonuclease Asp718

<400> 6  
cgcgggtacc aggtacagat ggtggcc

27

<210> 7  
<211> 34  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains a Bam HI site

<400> 7  
cgcgggatcc accatgaagg cttccagccg cttc

34

<210> 8  
<211> 58  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Contains complementary sequences to an Xba I site, translation stop codon, and an HA tag

<400> 8  
cgcgtctaga tcaagcgttag tctgggacgt cgtatggta gcctctgcac tcagcccc

58